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First Record of Genus *Phaeopholus* Roelofs, 1873 (Coleoptera: Curculionidae: Hyperinae) in Taiwan

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Abstract. *Phaeopholus* Roelofs, 1873 is a small genus composed of four species, known to be widely distributed in East Asia, but there is no formal record in Taiwan. This paper provides the first record of genus *Phaeopholus* in Taiwan, with two new distribution records for *P. ornatus* Roelofs, 1873 and *P. major* Roelofs, 1879. The partial COI sequences of both species and the photograph of habitus and male genitalia are provided.

Keywords: Hyperini, new faunistic record, weevil, DNA barcode

Introduction

The weevil genus *Phaeopholus* was established by Roelofs (1873) and traditionally belonged to the tribe Hyperini (Alonso-Zarazaga & Lyal, 1999; Alonso-Zarazaga et al., 2017). However, considering that the habitat preference of *Phaeopholus* is different from other members of Hyperini, Skuhrovec (2007) questioned the rational of this phylogenetic placement. Moreover, his morphological phylogenetic analysis suggested that this genus is closely related to Cepurini, rather than Hyperini. Although its phylogenetic placement is still controversial, most entomologists still treat it as a member of Hyperini (Legalov, 2011; Alonso-Zarazaga et al., 2017).

This genus currently consists of 4 species, including two species widely distributed in Japan and the Okinawa archipelago (*P. ornatus* Roelofs, 1873 and *P. major* Roelofs, 1879), and two species endemic to Fujian, China (*P. fuscocupreus* Voss, 1958, and *P. proximus* Voss, 1958)(Legalov, 2011; Alonso-Zarazaga et al., 2017). This genus can be distinguished from other Hyperini species by the combination of the following characters: body outline usually subglobular; rostrum elongate, at least twice as long as pronotum; antennal club elongate, four-segmented; elytra with interstriae slightly convex basally, without protruding tubercles; humeral angle rounded, contiguous with pronotal base (Oberprieler et al., 2014).

Although *Phaeopholus* has been widely recorded in East Asia, there is no formal record of this genus in Taiwan. During the examination of Taiwanese Curculionidae from field surveys and the museum collections, we found specimens of *Phaeopholus ornatus* and *P. major* from Taiwan for the first time. Herein, we provide the first formal record of genus *Phaeopholus* along with two new regional records in Taiwan. The partial COI gene sequences and illustration of habitus and male genitalia are also provided.

Materials and methods

The specimens were examined with a SMZ 800N stereomicroscope. The photograph was taken with a Olympus E-M5 Mark II digital camera with Olympus M. Zuiko Digital ED 60mm F2.8 Macro lens and edited using Photoshop CS6 and Helicon focus 6. Species identification follows the description of Roelofs (1879) and the key of Voss (1958), with the type series comparison of *P. ornatus* Roelofs, 1873 and *P. major* Roelofs, 1879. The specimens examined in this paper are deposited in the W.-Z. Tseng's private collection, Taichung, Taiwan (WZPCC), National Museum of Natural Science, Taichung, Taiwan (NMNS), Taiwan Agricultural Research Institute, Wufeng, Taichung, Taiwan (TARI), and Royal Belgian Institute of Natural Science, Brussels, Belgium (RBINS).

The total genomic DNA was extracted using FavorPrep™ tissue genomic DNA extraction mini kit (Favorgen, Pingtung, Taiwan) following the manufacturer's protocols. The partial sequence of cytochrome c oxidase subunit I (COI) gene was amplified by polymerase chain reaction (PCR) with primer-pair LCO1490/HCO2198 (Folmer et al., 1994). All the PCR products were purified and sequenced at National Yang Ming Chiao Tung University Cancer Progression Research Center (Taipei, Taiwan). Sequences

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were translated into amino acid and checked for stop codon in Geneious 11.0.5 (Kearse et al., 2012). All sequences are deposited in Genbank.

Results

***Phaeopholus ornatus* Roelofs, 1873**

絢麗圓葉象鼻蟲

(Figs 1–2, 5A–C)

Type material examined. Lectotype: JAPAN: 1♂, unknown, date unknown, W. Roelofs leg. (RBINS). **Paralectotype: JAPAN:** 1♂, unknown, date unknown, W. Roelofs leg. (RBINS); 2 ex, same data as lectotype (RBINS); 1♀, Hiller, Tokio, date unknown, W. Roelofs leg. (RBINS).

Other materials. TAIWAN: 1ex, Hueisun (惠蓀), Renai Township, Nantou County, 6. IX. 1987, S.-C. Tsaur leg. // NMNS ENT 7932-2015 (NMNS); 1ex, Dahanqiao (大漢橋), Fuxing Township, Taoyuan County, 21. IV. 1991, I.-S. Hsu leg. // NMNS ENT 7932-2013 (NMNS); 1ex, Jiabaotai (佳保台), Heping Township, Taichung County, 16. V. 1993, I.-S. Hsu leg. // NMNS ENT 7932-2006 (NMNS); 4ex, Yulao (宇老), Jianshi Township, Hsinchu County, 19. VI. 1993, I.-S. Hsu leg. // NMNS ENT 7932-2009; 7932-2010 (NMNS); 1ex, Meifeng (梅峰), Renai Township, Nantou County, 9. IV. 1998 – 19. V. 1998, C.-S. Lin & W.-T. Yang leg. // NMNS ENT 3243-599 (NMNS); 1ex, Chunyang (春陽), Renai Township, Nantou County, 19. II. 2002 – 12. III. 2002, C.-S. Lin & W.-T. Yang leg. // NMNS ENT 5237-630 (NMNS); 1ex, Meifeng (梅峰), Renai Township, Nantou County, 12. III. 2002 – 9. IV. 2002, C.-S. Lin & W.-T. Yang leg. // NMNS ENT 4912-24 (NMNS); 2ex, Chunyang (春陽), Renai Township, Nantou County, 9. IV. 2002 – 7. V. 2002, C.-S. Lin & W.-T. Yang leg. // NMNS ENT 5237-3273; 5237-3295 (NMNS); 2ex, Chunyang (春陽), Renai Township, Nantou County, 11. VI. 2002 – 9. VII. 2002, C.-S. Lin & W.-T. Yang leg. // NMNS ENT 5240-382; 5240-1099 (NMNS); 1ex, Kenting National Park (墾丁國家公園), Hengchun Township, Pingtung County, 16. II. 2005 – 17. II. 2005, C.-S. Lin & W.-T. Yang leg. // NMNS ENT 4810-373 (NMNS); 1ex, Chiupeng (九棚), Manzhou Township, Pingtung County, 20. XII. 2009 – 9. I. 2010, M.-L. Jeng & T.-R. Chen leg. // NMNS ENT 7104-383 (NMNS); 1♂, Hushan Hiking Trail (虎山親山步道), Xinyi District, Taipei City, 30. VII. 2017, W.-Z. Tseng leg. // WZPCC_00111 (WZPCC); 1♂, Shueiyuandi (水源地), 25°10'43.7844"N 121°27'56.0556"E, Tamsui District, New Taipei City, 16. IV. 2018, W.-Z. Tseng leg. // WZPCC_00215 (WZPCC); 1♂, Shueiyuandi (水源地), 25°10'39.6048"N 121°28'1.5348"E, Tamsui District, New Taipei City, 16. IV. 2018, W.-Z. Tseng leg. // WZPCC_00216 (WZPCC); 2♂♂3♀♀, Shueiyuandi (水源地), 25°10'39.0396"N 121°28'2.1864"E, Tamsui District, New Taipei City, 29. IV. 2018, W.-Z. Tseng leg. // WZPCC_00220 – WZPCC_00224 (WZPCC).

Diagnosis. Body length less than 3 mm (more than 3.5 mm in *P. major* and *P. fuscocupreus*); pronotum with median furrow (absent in *P. proximus*); upper margin of pronotum weakly sinuated (Figs 5A–B) (strongly sinuated, truncate medially and laterally in *P. major* and *P. fuscocupreus*); black longitudinal tubercle on the base of interstria III and V and black transverse mark between base of interstria II-V (black mark only shows on base of interstria III in *P. proximus*); pronotum and venter with metallic green scales, (Fig. 5C) (grey scales in *P. major*; light brown, lustrous metallic in *P. proximus*; dark brown, lustrous metallic in *P. fuscocupreus*); pedon apex in dorsal view broaden, rectangular (rounded in *P. major*), apodeme of penis as long as pedon, (Figs 2A–B) (longer than pedon in *P. major*).

Distribution. China (Fujian province); Japan (Honshu, Shikoku, Kyushu, Okinawa, Tokunoshima Islandand Izu Island); South Korea (Kojima & Morimoto, 2004; Kojima & Kaga, 2011; Alonso-Zarazaga et al., 2017); Taiwan (new record).

GenBank accession number. WZPCC_00216: MW806916.

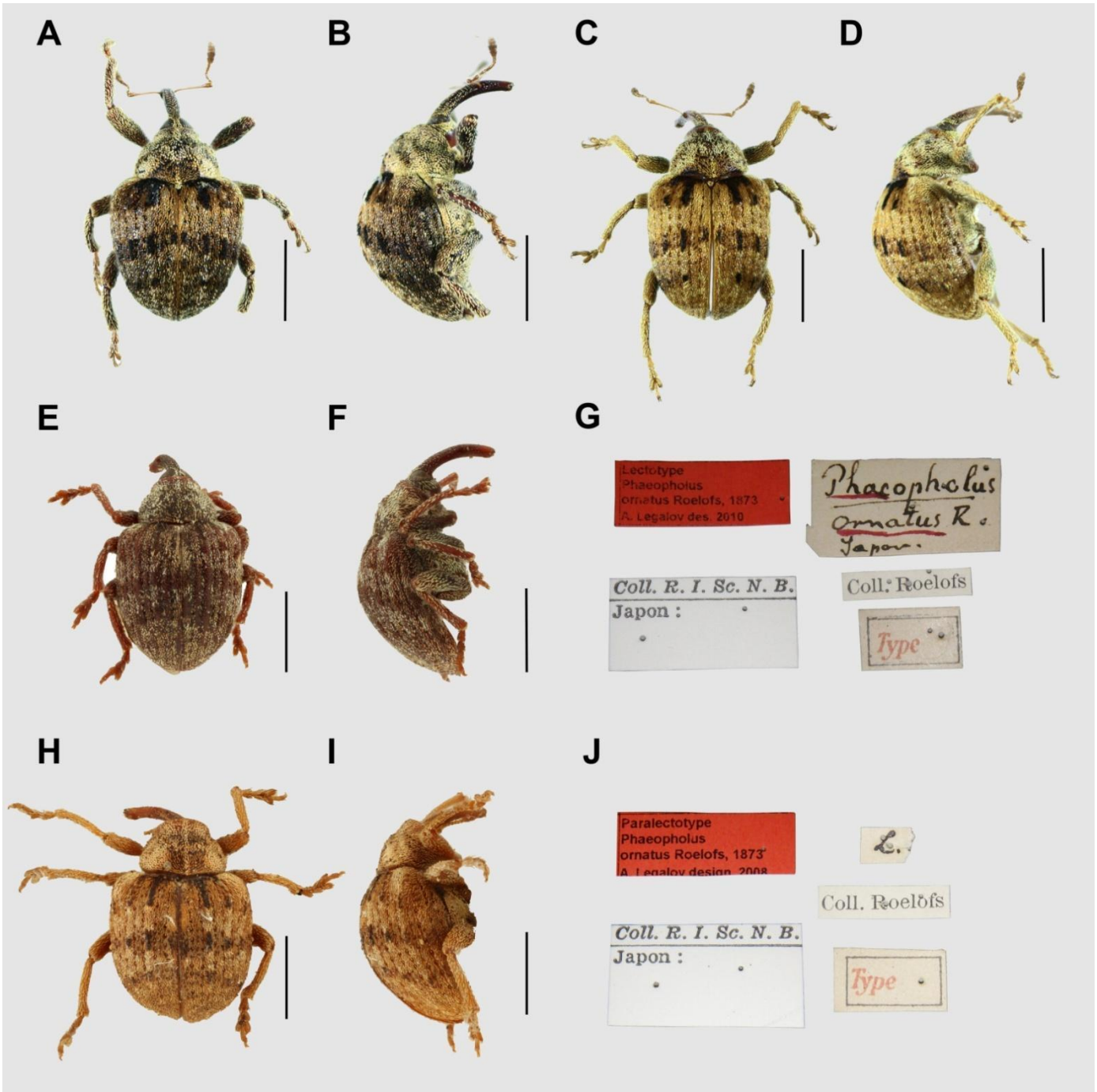

Figure 1. Habitus of *Phaeopholus ornatus* Roelofs, 1873. A: male, dorsal view, B: male, lateral view. C: female, dorsal view, D: female, lateral view. E: Lectotype, male, dorsal view, F: Lectotype, male, lateral view, G: Lectotype, labels. H: Paralectotype, male, dorsal view, I: Paralectotype, male, lateral view, J: Paralectotype, labels. Scale bar: 1mm.

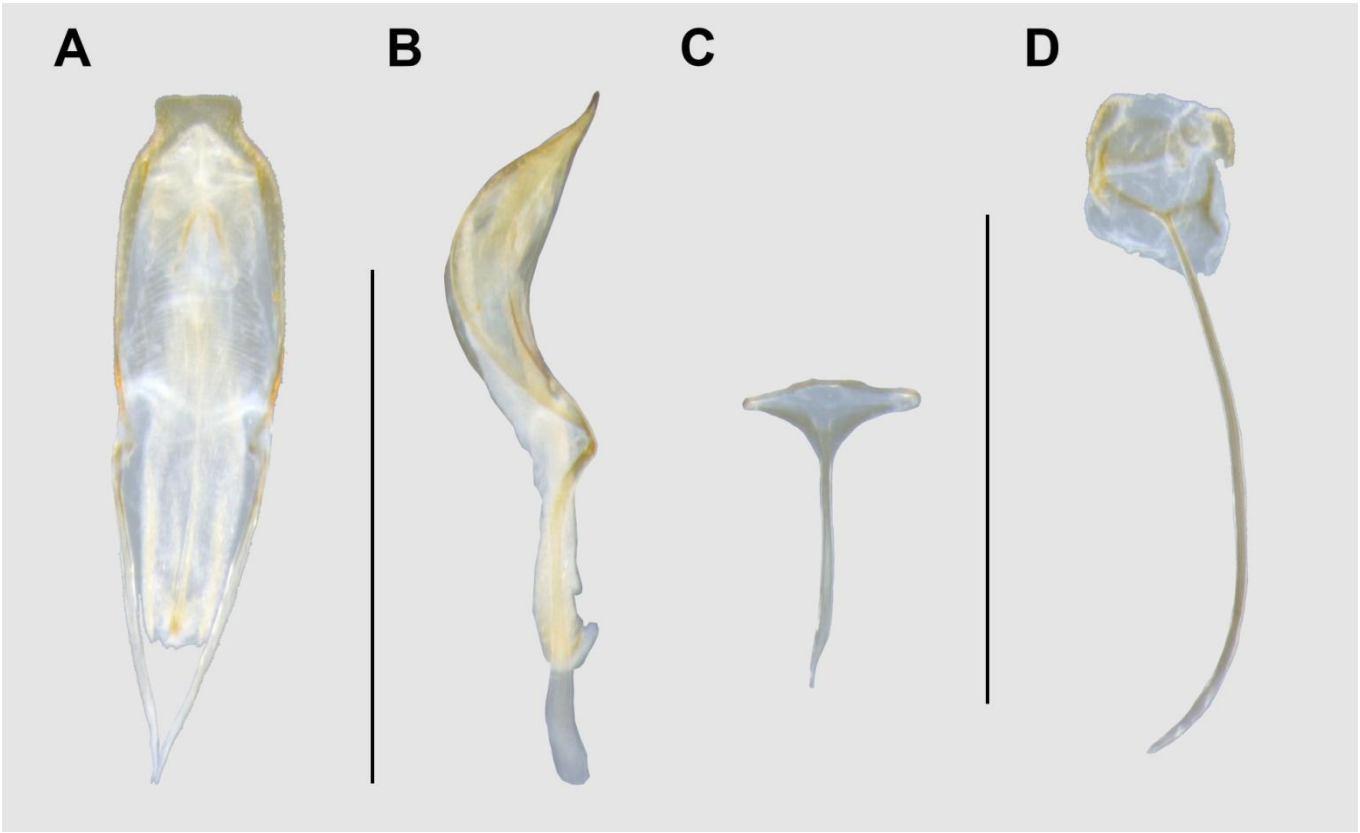

Figure 2. Male genitalia of *Phaeopholus ornatus* Roelofs, 1873. A: penis, dorsal view, B: penis, lateral view. C: tegmen ring, dorsal view, D: tegmen ring, lateral view. Scale bar: 1mm.

***Phaeopholus major* Roelofs, 1879**

巨圓葉象鼻蟲

(Figs 3–4, 5: D–F)

Type material examined. Lectotype: JAPAN: 1♀, Hiller, Tokio, date unknown, W. Roelofs leg. (RBINS).
Other materials. TAIWAN: 1♀, Hewangshan (合望山), Renai Township, Nantou County, 30. IV. 1989, C.-C. Lo leg. // NMNS ENT 7932-2014 (NMNS); 1♂, Bilu (碧綠), Xiulin Township, Hualien County, 26. V. 1991, C.-L. Li leg. // NMNS ENT 7932-2012 (NMNS); 1♀, Meifeng (梅峰), Renai Township, Nantou County, 10. XII. 2002 – 7. I. 2003, C.-S. Lin & W.-T. Yang leg. // NMNS ENT 6096-12 (NMNS); 1♀, Kenting National Park (墾丁國家公園), Hengchun Township, Pingtung County, 13. V. 2004 – 14. V. 2004, C.-S. Lin & W.-T. Yang leg. // NMNS ENT 4409-1474 (NMNS); 1♂, Kenting National Park (墾丁國家公園), Hengchun Township, Pingtung County, 16. II. 2005 – 17. II. 2005, C.-S. Lin & W.-T. Yang leg. // NMNS ENT 4810-392 (NMNS); 1♂, Meifeng (梅峰), Renai Township, Nantou County, 17. X. 2006 – 14. XI. 2006, C.-S. Lin & W.-T. Yang leg. // NMNS ENT 7512-84 (NMNS); 1♀, Machia (瑪家), Pingtung County, 25. V. 2016, Y.-T. Chung leg. // WZPCC_00480M (TARI); 1♀, Wuchihshan (五指山), Zhudong Township, Hsinchu County, 9. XII. 2008, S.-F. Yu leg. // WZPCC_00483M (TARI).

Diagnosis. Body length more than 3.5 mm (less than 3.5 mm in *P. ornatus* and *P. proximus*); upper margin of pronotum strongly sinuated, truncate medially and laterally (Figs 5D–E)(weakly sinuated in *P. ornatus* and *P. proximus*); pronotum and venter with grey scales (Fig. 5F)(metallic green in *P. ornatus*; light brown, metallic lustrous in *P. proximus*; dark brown, lustrous metallic in *P. fuscocupreus*); pedon apex in dorsal view rounded (broader in *P. ornatus*), apodeme of penis 1.5× longer than pedon, (Figs 4A–B (as long as pedon in *P. ornatus*).

Distribution. Japan (Honshu, Shikoku, Kyushu and Tsushima Island); South Korea (Kojima & Morimoto, 2004; Kojima & Kaga, 2011; Alonso-Zarazaga et al., 2017); Taiwan (new record).

GenBank accession number. WZPCC_00480M: MW806915.

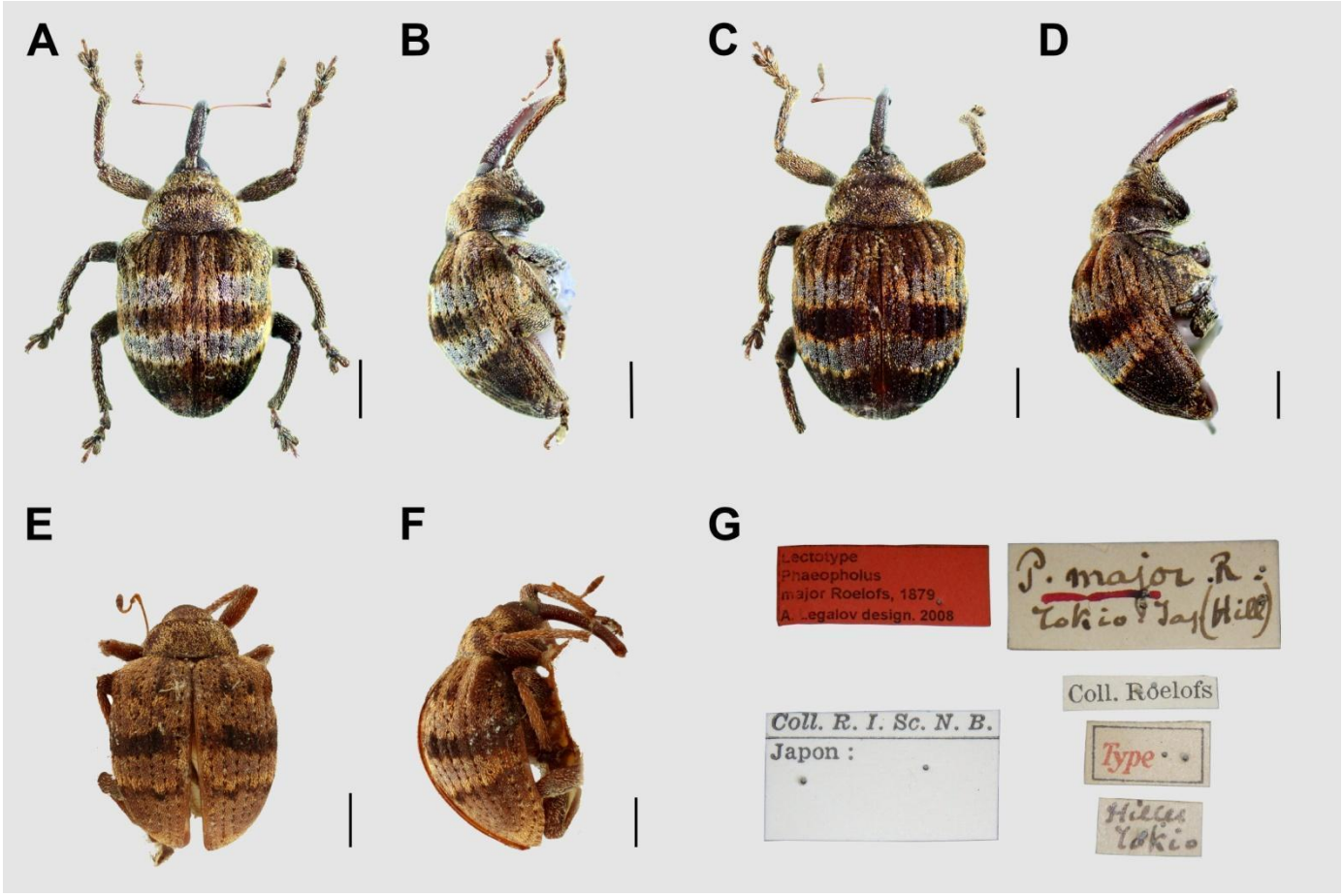

Figure 3. Habitus of *Phaeopholus major* Roelofs, 1879. A: male, dorsal view, B: male, lateral view. C: female, dorsal view, D: female, lateral view. E: Lectotype, female, dorsal view, F: Lectotype, female, lateral view, G: Lectotype, labels. Scale bar: 1mm.

Figure 4. Male genitalia of *Phaeopholus major* Roelofs, 1879. A: penis, dorsal view, B: penis, lateral view. C: tegmen ring, dorsal view, D: tegmen ring, lateral view. Scale bar: 1mm.

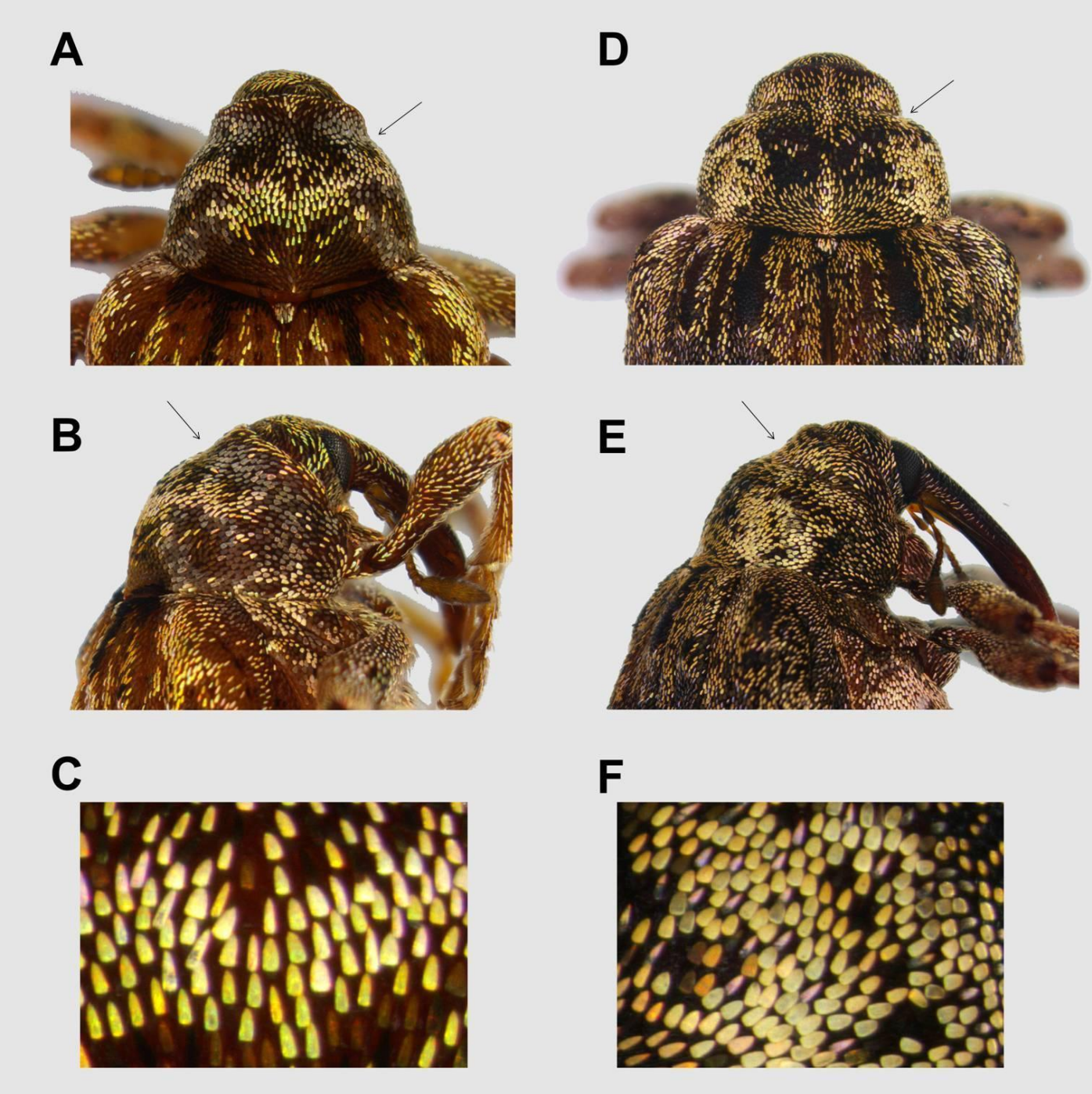

Figure 5. Diagnostic characters of *Phaeopholus* in Taiwan. A–C: *Phaeopholus ornatus* Roelofs, 1873. A: pronotum, dorsal view, B: pronotum, lateral view, C: pronotal scales. D–F: *Phaeopholus major* Roelofs, 1879. D: pronotum, dorsal view, E: pronotum, lateral view, F: pronotal scales.

Acknowledgments

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臺灣新紀錄圓葉象鼻蟲屬記述（鞘翅目：象鼻蟲科：葉象鼻蟲亞科）

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摘要: 圓葉象鼻蟲屬 (*Phaeopholus* Roelof, 1873) 先前已知廣泛分布在東亞地區，然而臺灣尚無正式的分布紀錄。本研究提供本屬於臺灣的新分布紀錄，並鑑定出兩物種絢麗圓葉象鼻蟲 (*P. ornatus* Roelofs, 1873) 及巨圓葉象鼻蟲 (*P. major* Roelofs, 1879)，本文亦提供兩物種的部分粒線體遺傳資訊與標本形態及雄性生殖器照片。

關鍵詞: 葉象鼻蟲族、新紀錄、象鼻蟲、生命條碼

[研究文章 Research Article]

http://zoobank.org/urn:lsid:zoobank.org:pub:BD853C3D-DA8F-43FC-9B29-BB9FBCD7F0D8

A Preliminary Phylogenetic Study on the Systematics of *Lycocerus* Gorham (Coleoptera: Cantharidae)

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Abstract. The genus *Lycocerus* Gorham, 1889 is a highly speciose group of Asian soldier beetles. Okushima (2005) divided this genus into several species groups and presumed their potential phylogenetic relationship based on anatomical comparison, and a few more species groups were subsequently proposed by various authors. In this study, I reinvestigated the relationship within *Lycocerus* using phylogenetic analyses of morphological data and extended the taxa sampling to corroborate all currently known major lineages. The resulting topology only partially agrees with Okushima (2005), but supports the synonymy of *Athemus* Lewis, 1895, *Athemellus* Wittmer, 1972, *Mikadocantharis* Wittmer & Magis, 1978, *Andrathemus* Wittmer, 1978 and *lsathemus* Wittmer, 1995 with *Lycocerus*.

Key word: Soldier beetles, Cantharinae, systematics, morphological phylogenetics, Asia

Introduction

Cantharidae is a diverse elateroid beetle family with a brightly colored soft-body, originating from the Late Jurassic and maintaining the high rate of diversification since then (McKenna et al., 2019). *Lycocerus* Gorham, 1889 is a highly species-rich Asian genus of soldier beetles, with more than 300 species distributed in the Oriental and eastern Palaearctic regions (Kazantsev & Brancucci, 2007). Okushima (2005) revised the Japanese fauna and summarized nine major species groups with a couple of subgroups based on both external and genitalic characters. Subsequently, four species groups of *Lycocerus* were established, including the *L. michiakii* Group based on species from Laos (Okushima & Brancucci, 2008), the *L. hickeri* Group based on species from China and Vietnam (Yang et al., 2014), the *L. rhagonychiformis* Group based on the Taiwanese species (Hsiao & Okushima, 2016), and the *L. fainanus* Group based on species from China, Taiwan and Vietnam (Okushima & Hsiao, 2017).

Currently, most research on *Lycocerus* was predominantly focused on the alpha and beta taxonomy, with only few studies attempting to approach the issues of systematics. Okushima (2005) assumed the phylogeny of *Lycocerus* based on the comparative anatomy, and Hsiao et al. (2016) attempted to reconstruct the *Lycocerus* phylogeny using a cladistics analysis based on 29 adult traits and geographic distribution, covering all proposed species groups. Nonetheless, the main purpose of the phylogenetic analysis in Hsiao et al. (2016) aimed to clarify the systematic placement of some species related to the *L. hanatanii* Group and the relationship among most species groups was unresolved. In the present study, I reanalyze the relationship within *Lycocerus* to examine the phylogenetic hypothesis in Okushima (2005). Also, I include all genera and subgenera synonymized with *Lycocerus* by Okushima (2005) to test this taxonomic treatment.

Material and methods

Taxon sampling and character selection

The ingroup contained 15 species, representing all known species groups (Table 1). *Lycocerus pallidulus* (Wittmer) of *L. maculicollis* Group and *L. japonicus* (Kiesenwetter) of *L. lineatipennis* Group were also selected representing *lsathemus* Wittmer and *Mikadocantharis* Wittmer & Magis. Two species of *Themus* Motschulsky, namely *Th.* (*Th.*) *nobilis nobilis* (Gorham) and *Th.* (*Telephorops*) *sauteri* (Pic), were used as outgroups.

The data matrixes from Okushima (2005) and Hsiao et al. (2016) were used as a starting point for morphological character coding. After reconsideration of characters used in previous phylogenies of *Lycocerus*, 21 characters were kept, seven were amended, four were added and one was deleted to obtain a matrix pertinent to the taxa included in analyses. No geographic character was used. In total, 46 adult characters were coded for the phylogenetic analysis (Tables 2, 3). I assembled the matrix using MESQUITE v. 3.61 (Maddison & Maddison, 2019). Inapplicable data were scored as '-' in the character matrix.

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Table 1. Taxa included in the phylogenetic analysis.

	Genus/Subgenus	Species	Species group	Genus/Subgenus sensu Wittmer
Outgroup	*Themus* (*Themus*)	*Th*. (*Th*.) *nobilis nobilis* (Gorham)	-	-
	Themus (*Telephorops*)	*Th*. (*Telephorops*) *sauteri* (Pic)	-	-
Ingroup	*Lycocerus*	*L. maculicollis* (Hope)	*L. maculicollis* Group	*Lycocerus*
		L. pallidulus (Wittmer)	*L. maculicollis* Group	*Athemus* (*Isathemus*)
		L. japonicus (Kiesenwetter)	*L. lineatipennis* Group	*Athemus* (*Mikadocantharis*)
		L. yamatensis Okushima	*L. lineatipennis* Group	*Athemus* (*Andrathemus*)
		L. purpureus Kazantsev	*L. purpureus* Group	*Athemus* (*Andrathemus*)
		L. vitellinus (Kiesenwetter)	*L. vitellinus* Group	*Athemus* (*Andrathemus*)
		L. aegrotus (Kiesenwetter)	*L. aegrotus* Group	*Athemus* (*Athemus*)
		L. masatakai Okushima	*L. fainanus* Group	*Athemus* (*Athemus*)
		L. michiakii Okushima & Brancucci	*L. michiakii* Group	*Athemus* (*Athemus*)
		L. suturellus suturellus (Motschulsky)	*L. suturellus* Group	*Athemus* (*Athemus*)
		L. adusticollis (Kiesenwetter)	*L. adusticollis* Group	*Athemus* (*Athemellus*)
		L. hanatanii (Okushima)	*L. hanatanii* Group	*Athemus* (*Athemellus*)
		L. rhagonychiformis (Wittmer)	*L. rhagonychiformis* Group	*Athemus* (*Athemellus*)
		L. sichuanus Y. Yang & X. Yang	*L. hickeri* Group	*Athemus* (*Athemellus*)
		L. watanabei (Ishida & M. Satô)	*L. oedemeroides* Group	*Athemus* (*Athemellus*)

Table 2. Character matrix used for the phylogenetic analysis of *Lycocerus*.

Taxa \ Characters	0000000000111111111122222222233333333334444444 0123456789012345678901234567890123456789012345
Themus nobilis nobilis	201101000000-0110121100000000000000000000-0-0-0
Themus sauteri	201101000000-0110021000000000000000010200-0-0-0
Lycocerus maculicollis	20011010000100111110000000010100011002010101000
Lycocerus suturellus suturellus	21000110011111111110110000000101000110021101010 0
Lycocerus vitellinus	11000120011111111110111010001010001101201010100
Lycocerus purpureus	00110000011101110101110100010100011002010101 11
Lycocerus adusticollis	11000110011111111110110000000000001100201110100
Lycocerus yamatensis	11000120011111111110111010001010001100201010100
Lycocerus watanabei	11000110011111011101100000010100011002110 11100
Lycocerus aegrotus	22000010011111111110110000000000001100201011110
Lycocerus michiakii	12000110011111101131100000010100011002011101 00
Lycocerus sichuanus	12000110011101111101110100010100011002010101 00
Lycocerus rhagonychiformis	01000011111111011101100000000000001100111011100
Lycocerus hanatanii	01110021111111011101100000000000001110111011100
Lycocerus masatakai	22000110011111110101100000010100011012010101 00
Lycocerus pallidulus	11000010011111111110111111101111101100201010100
Lycocerus japonicus	11100120011111111110111111111111111100201010110

Table 3. List of characters and states used in the phylogenetic analysis.

0	Body size	0. small (5-7mm) 1. medium (8-10mm) 2. large (> 10mm)
1	Body form judged on the ratio of the length to the width at the widest part of the conjoint elytra	0. stout (about 2.2) 1. middle (2.5-3.0) 2. slender (mainly greater than 3.0)
2	Antennal length in males	0. exceeding 1/2 elytral length 1. extending to 1/2 elytral length
3	Antennal length in females	0. extending to 1/2 of elytral length 1. barely exceeding the humeri, but not extending to 1/2 elytral length
4	Antennae	0. filiform 1. serrate
5	Grooves on antennal segments in male	0. absent 1. present
6	Terminal maxillary palpomere	0. stout; Hsiao et al., 2016: Fig. 1A 1. subtriangular; Hsiao et al., 2016: Fig. 1B 2. slender; Hsiao et al., 2016: Fig. 1C
7	Eyes	0. large; Hsiao et al., 2016: Fig. 1D 1. small; Hsiao et al., 2016: Fig. 1E
8	Eyes	0. prominent; Hsiao et al., 2016: Fig. 1D 1. not very prominent; Hsiao et al., 2016: Fig. 1E
9	Vertex	0. flat 1. faintly hollowed
10	Vertex	0. smooth 1. distinctly punctate
11	Pronotum	0. disc-shaped, distinctly expanded; Hsiao et al., 2016: Fig. 1H 1. normal, trapezoid or subquadrate, not expanded as above

12	If pronotum not distinctly expanded	0. trapezoid; Hsiao et al., 2016: Fig. 1F 1. subquadrate; Hsiao et al., 2016: Fig. 1G
13	Greatest width of pronotum in male	0. wider than head 1. nearly as wide as head or narrower than head
14	Angular convexity on pronotum	0. distinct; Hsiao et al., 2016: Fig. 1G 1. indistinct
15	Elytra	0. Shortened, with abdomen largely exposed 1. entirely covered abdomen
16	Elytra	0. with strong metallic lustre 1. lusterless or semi-lustrous
17	Elytra	0. strongly depressed 1. normal
18	Elytra	0. subparallel at the sides 1. apically expanded 2. moderately narrowed apically 3. strongly narrowed apically
19	Costae on elytra	0. distinct 1. hardly recognizable
20	Legs	0. stout; Hsiao et al., 2016: Fig. 1I 1. slender; Hsiao et al., 2016: Fig. 1J
21	Outer claws of forelegs in male	0. simple 1. with tooth/lobe
22	Inner claws of forelegs in male	0. simple 1. with tooth/lobe
23	Outer claws of mid legs in male	0. simple 1. with tooth/lobe
24	Inner claws of mid legs in male	0. simple 1. with tooth/lobe
25	Outer claws of hind legs in male	0. simple 1. with tooth/lobe
26	Inner claws of hind legs in male	0. simple 1. with tooth/lobe
27	Outer claws of forelegs in female	0. simple 1. with tooth/lobe
28	Inner claws of forelegs in female	0. simple 1. with tooth/lobe
29	Outer claws of mid legs in female	0. simple 1. with tooth/lobe
30	Inner claws of mid legs in female	0. simple 1. with tooth/lobe
31	Outer claws of hind legs in female	0. simple 1. with tooth/lobe
32	Inner claws of hind legs in female	0. simple 1. with tooth/lobe

33	Dorsal plate of each paramere of aedeagus	0. fused or nearly fused 1. separated
34	Laterophyses of aedeagus	0. nearly fused 1. widely separated on both sides of median lobe
35	Laterophyses of aedeagus	0. long, distinctly visible in lateral view 1. short, barely visible or invisible in lateral view
36	Median lobe of aedeagus	0. simple 1. provided with a process dorsad
37	Apical part of median lobe of aedeagus	0. widened apically 1. strongly narrowed apically 2. moderately narrowed apically
38	Apical part of vagina	0. broad 1. extended apically as a thick duct
39	Diverticulum	0. thick 1. thin
40	If diverticulum thin	0. long 1. short
41	Spermathecal duct	0. absent 1. present
42	If spermathecal duct present	0. spermathecal duct short 1. spermathecal duct long
43	Spermatheca	0. short, sac-shaped 1. long and thin, provided with spiral tube(s)
44	If spermatheca long and thin	0. with a spiral tube 1. with two spiral tubes
45	Accessory gland	0. simple (thin, filiform) 1. modified (abruptly expanded)

Maximum Parsimony

Maximum parsimony (MP) analysis was carried out in TNT ver. 1.5 (Goloboff & Catalano, 2016), using the implicit enumeration search with all characters unordered and unweighted. The assembled data matrix was also analyzed under the implied weighting (Goloboff et al., 2017) using the same algorithm to resolve the previously unresolved relationship (i.e., polytomy). I investigated the sensitivity of clades to alternative character weighting schemes and the impact of strong to light downweighing of homoplastic characters on the inferred trees was examined by running implied weighting analyses under K values 3, 10 and 21 respectively. Character states were mapped on the most parsimonious tree using Winclada ver. 1.0 (Nixon, 2002), showing only unambiguous changes. Bootstrap (BS) support values were calculated with 2000 replicates in TNT ver. 1.5, with an 'absolute frequencies' option, to indicate the statistical support for each hypothesised clade (Felsenstein, 1985). Nodes with bootstrap values <50% were considered to be unsupported and not shown.

Bayesian inference

Bayesian inference (BI) was conducted using MrBayes 3.2.6 (Ronquist et al., 2012). The Mkv model was used with a gamma distribution. Two Markov chain Monte Carlo runs (MCMC) were executed with four chains for 5 million generations. The first 25% of trees were discarded as burn-in. Convergence was assessed by checking that all parameters had reached sufficient effective sample sizes (> 200) and by comparing results from two independent runs using Tracer v1.7.0 (Rambaut et al., 2018). Nodes with posterior probability (PP) > 0.95 were considered to be strongly supported, with PP = 0.90–0.94 moderately supported, with PP = 0.85–0.89 weakly supported, and PP < 0.85 unsupported according to Żyła et al. (2017). The 50% majority-rule consensus (MRC) tree was rooted with *Th.* (*Th.*) *nobilis nobilis* + *Th.* (*Te.*) *sauteri*. Additionally, I followed Zhou et al. (2019) to obtain the maximum clade credibility (MCC) tree from post burn-in trees (ESS > 200) by using Treeannotator (Bouckaert et al., 2014). The tree was displayed and edited in FigTree v1.4.3 (https://github.com/rambaut/figtree/).

Maximum Likelihood

Maximum Likelihood (ML) phylogenetic reconstruction was performed using the web version of IQ-TREE (ver. 1.6.11, see http://www.iqtree.org/; Nguyen et al., 2015; Trifinopoulos et al., 2016). The prior substitution model was estimated by Model Finder (Kalyaanamoorthy et al., 2017) implemented in the same software for morphological data. Nodal support was estimated using an ultrafast bootstrap analysis with 1000 replicates and single branch test was obtained by SH-aLRT branch test with 1000 replicates, where BS values ≥ 80% are clades supported (Guindon et al., 2010). The resulting phylogenetic tree was rooted with *Th.* (*Th.*) *nobilis nobilis* + *Th.* (*Te.*) *sauteri* and displayed in FigTree v1.4.3 as above.

Results

MP, BI and ML analyses of the entire matrix produced highly concordant topologies (Figs. 1–4). Implicit enumeration search under the equal weighting in the MP analysis of the taxa sampling with exclusion of *L. pallidulus* and *L. japonicus* resulted in 9 most parsimonious trees (tree length (L) = 87 steps, consistency index (CI) = 59, retention index = 63). The majority consensus tree (L = 87; CI = 59; RI = 63; Fig. 1), recovering monophyletic (99% BS) *Lycocerus* as synapomorphically supported by the not expanded pronotum (11:1), subparallel-sided elytra (18:1), simple outer claws of forelegs in female (27:1), simple outer claws of mid legs in female (29:1), separated dorsal plate of each paramere of aedeagus (33:1), widely separated laterophyses of aedeagus (34:1), thin diverticulum (39:1), spermathecal duct present (41:1) and long and thin spermatheca, with spiral tube(s) (43:1), but the relationship among crown groups was not resolved. The sister relationships between *L. pallidulus* (*L. maculicollis* Group: *L. pallidulus* Subgroup) and *L. japonicus* (*L. lineatipennis* Group: *L. japonicus* Subgroup), and between the *L. hanatanii* Group and the *L. rhagonychiformis* Group were supported, with 93% BS and 95% BS, respectively.

MP analysis of the same dataset under the implied weighting using various K values resulted in 9 most parsimonious trees when K=3 (strong downweighing impact of homoplasic characters) and 3 trees when K=10 and 21 (moderate to light downweighing impact). The respective majority consensus trees show highly consistent topologies, with minor differences in placement of few taxa, resolving the polytomy in previous analysis under the equal weighting (Fig. 2), which suggests the relationship *L. maculicollis* Group + (*L. aegrotus* Group + (*L. fainanus* Group + ((*L. suturellus* Group + (*L. oedemeroides* Group + (*L. rhagonychiformis* Group + *L. hanatanii* Group))) + ((*L. adusticollis* Group + *L. michiakii* Group) + ((*L. purpurascens* Group + *L. hickeri* Group) + ((*L. pallidulus* Subgroup + *L. japonicus* Subgroup) + (*L. vitellinus* Group + *L. lineatipennis* Group))))))) (L = 88; CI = 59; RI = 62) or *L. maculicollis* Group + (*L. purpurascens* Group + (*L. fainanus* Group + ((*L. suturellus* Group + (*L. oedemeroides* Group + (*L. aegrotus* Group + (*L. rhagonychiformis* Group + *L. hanatanii* Group)))) + ((*L. adusticollis* Group + *L. michiakii* Group) + (*L. hickeri* Group + ((*L. pallidulus* Subgroup + *L. japonicus* Subgroup) + (*L. vitellinus* Group + *L. lineatipennis* Group))))))) (L = 87; CI = 59; RI = 63) within *Lycocerus*.

In the BI analysis, the majority-rule consensus tree strongly supports a monophyletic *Lycocerus* (PP = 1.00), and the clade containing all species groups except for the *L. maculicollis* Group and the clade including the *L. purpurascens* Group, *L. hickeri* Group, *L. pallidulus* Subgroup, *L. japonicus* Subgroup, *L. vitellinus* Group and *L. lineatipennis* Group are weakly supported, respectively. The affinities between the *L. rhagonychiformis* Group and *L. hanatanii* Group, and between *L. pallidulus* Subgroup and *L. japonicus* Subgroup are also strongly supported as MP analysis recovered. Nonetheless, the relationships among most of the species groups were not well resolved (Fig. 3A). The maximum clade credibility tree presents a well-resolved topology nearly consistent with the majority consensus tree produced by the MP analysis under the implied weighting using K = 3 (Fig. 3B).

The ML tree also recovered the strongly supported monophyletic *Lycocerus* (100% BS). The monophyly of the clade including all species groups except for *L. maculicollis* Group is supported (80% BS). ML tree also supported the following sister relationships: *L. rhagonychiformis* Group + *L. hanatanii* Group (100% BS), *L. vitellinus* Group + *L. lineatipennis* Group (86% BS) and (*L. pallidulus* Subgroup + *L. japonicus* Subgroup (98% BS) (Fig. 4).

Discussion

Okushima (2005) proposed the potential phylogenetic relationship of the main species groups based on 18 adult characteristics, suggesting the relationship (*L. oedemeroides* Group + (*L. aegrotus* Group + *L. hanatanii* Group)) + ((*L. adusticollis* Group + *L. lineatipennis* Group) + (*L. purpurascens* Group + (*L. vitellinus* Group + (*L. maculicollis* Group + *L. suturellus* Group)))). The present study increases the taxa sampling from 9 species groups to 13 species groups (including 4 currently established groups) and 2 additional subgroups, representing main lineages of this taxonomically diverse genus, and the analyses using various methods (i.e. MP, BI and ML) resulted in generally consistent topologies (Figs. 1–4). My results provide a new perspective to the *Lycocerus* phylogeny in contrast to most of the clades suggested in Okushima (2005). Nevertheless, the close affinity among *L. aegrotus* Group, *L. hanatanii* Group and *L. oedemeroides* Group presumed by Okushima (2005) is recovered in my results.

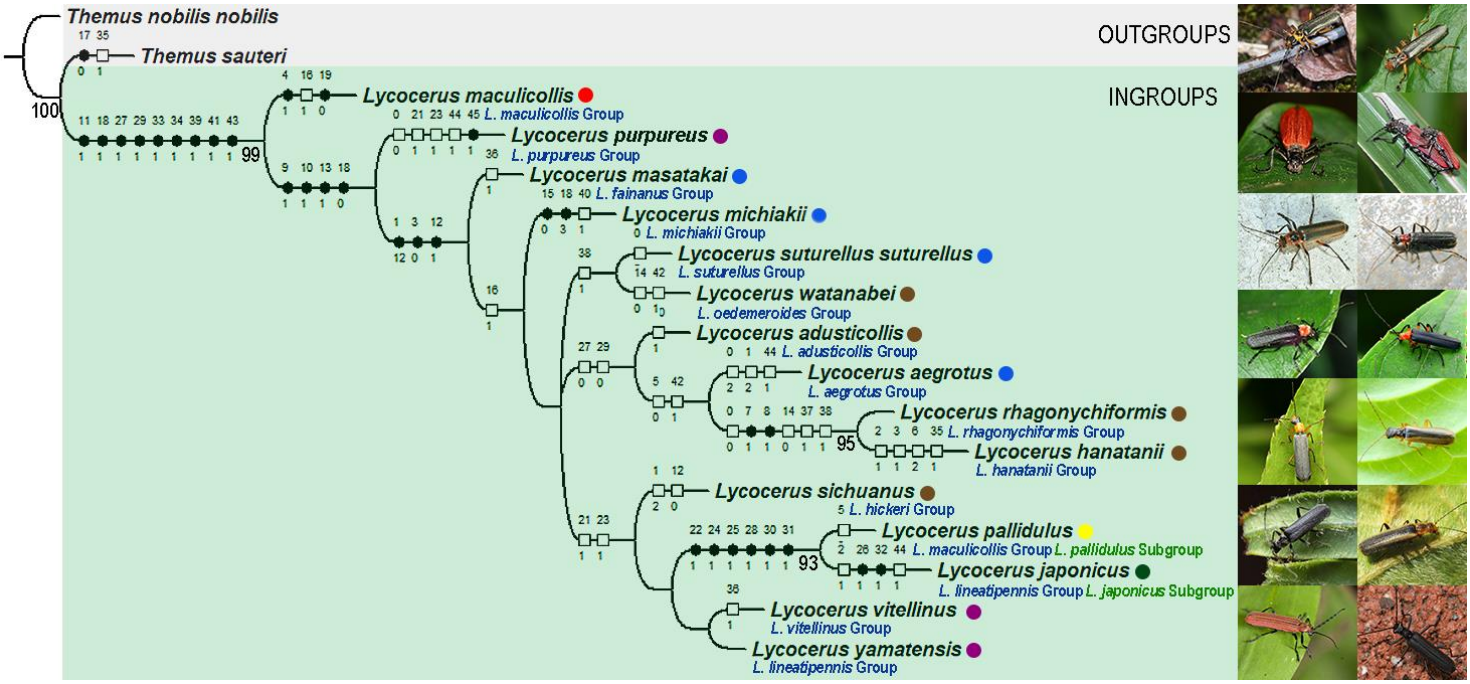

Figure 1. The majority consensus tree of 9 most parsimonious trees of diverse *Lycocerus* Gorham obtained by implicit enumeration search under equal weighting (L = 87; CI = 59; RI = 63). Black circles indicate synapomorphies; white rectangles indicate parallelisms or reversals; character numbers are given above circles, and character states are labelled below circles. Bootstrap values (BS > 49%) are shown near each of the corresponding nodes. Circles after species names indicate the genus/subgenus based on Wittmer's classification, showing the non-monophyly: red circle: *Lycocerus*; blue circles: *Athemus* (*Athemus*); brown circles: *Athemus* (*Athemellus*); purple circles: *Athemus* (*Andrathemus*); yellow circles: *Athemus* (*lsathemus*); dark green circles: *Athemus* (*Mikadocantharis*).

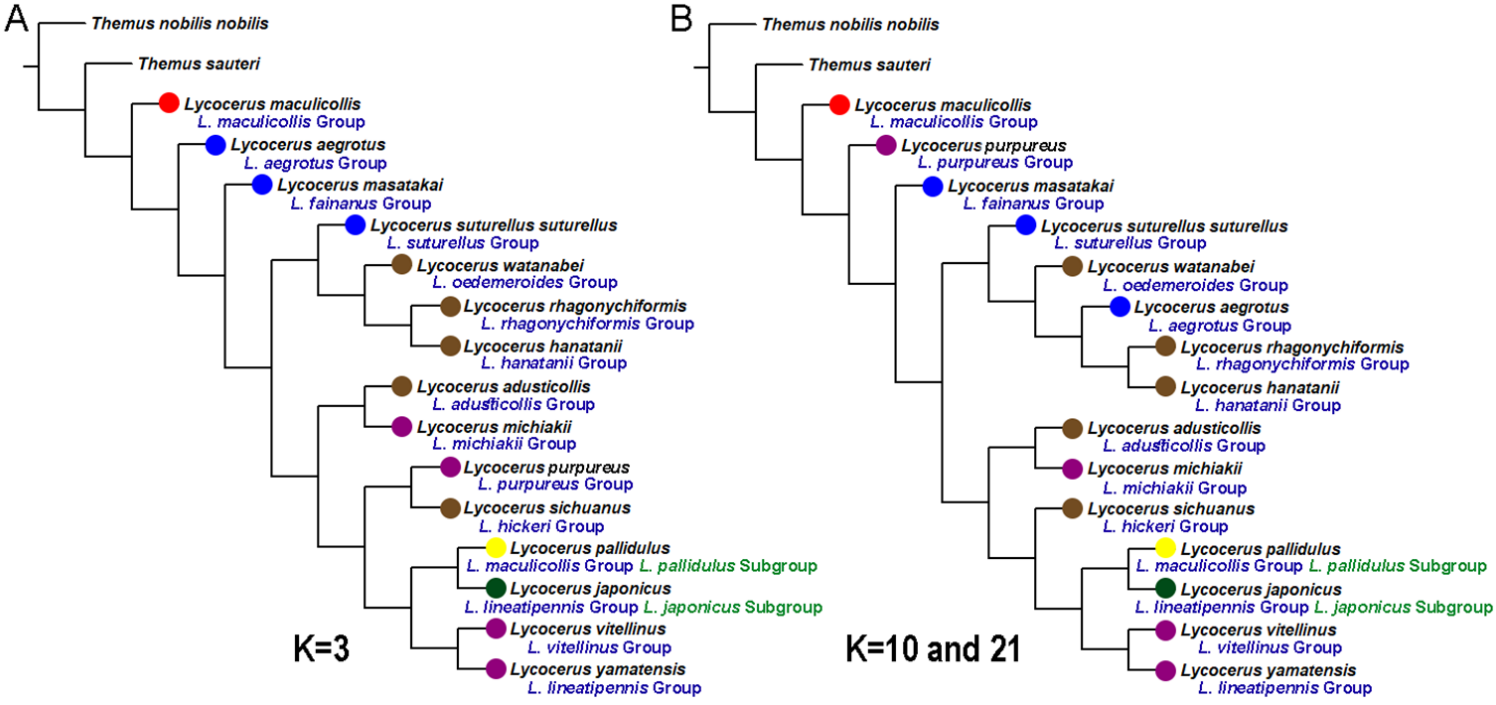

Figure 2. Phylogenies inferred from Maximum Parsimony under implied weighting. A - the majority consensus tree of 9 most parsimonious trees when K = 3 (L = 88; CI = 59; RI = 62); B - the majority consensus tree of 3 most parsimonious trees when K = 10 and 21 (L = 87; CI = 59; RI = 63). Circles after species names indicate the genus/subgenus based on Wittmer's classification, showing the non-monophyly: red circle: *Lycocerus*; blue circles: *Athemus* (*Athemus*); brown circles: *Athemus* (*Athemellus*); purple circles: *Athemus* (*Andrathemus*); yellow circles: *Athemus* (*lsathemus*); dark green circles: *Athemus* (*Mikadocantharis*).

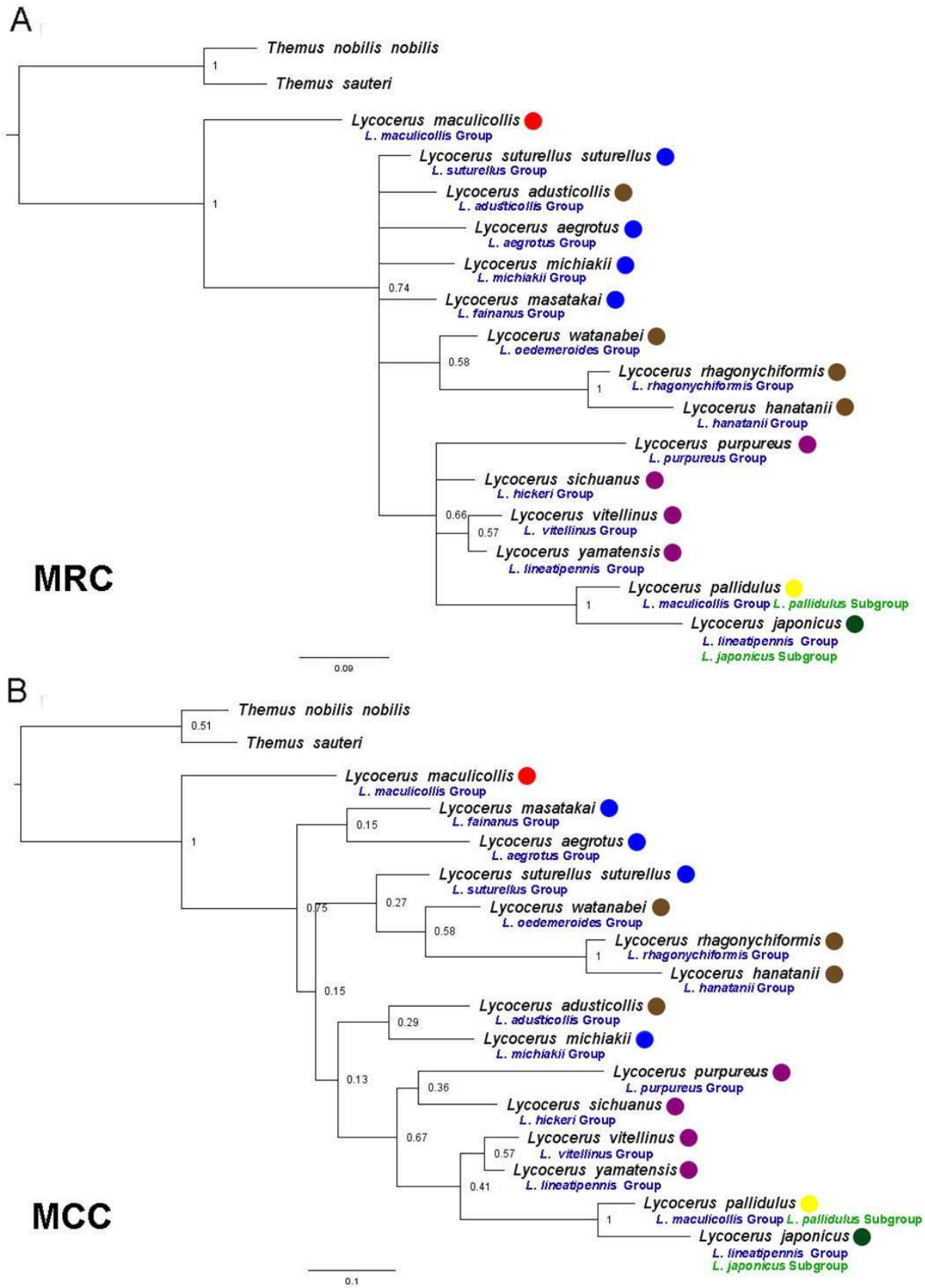

Figure 3. Phylogenies inferred from Bayesian inference. A – the 50% majority-rule consensus tree; B – the maximum clade credibility tree. Circles after species names indicate the genus/subgenus based on Wittmer's classification, showing the non-monophyly: red circle: *Lycocerus*; blue circles: *Athemus* (*Athemus*); brown circles: *Athemus* (*Athemellus*); purple circles: *Athemus* (*Andrathemus*); yellow circles: *Athemus* (*Isathemus*); dark green circles: *Athemus* (*Mikadocantharis*).

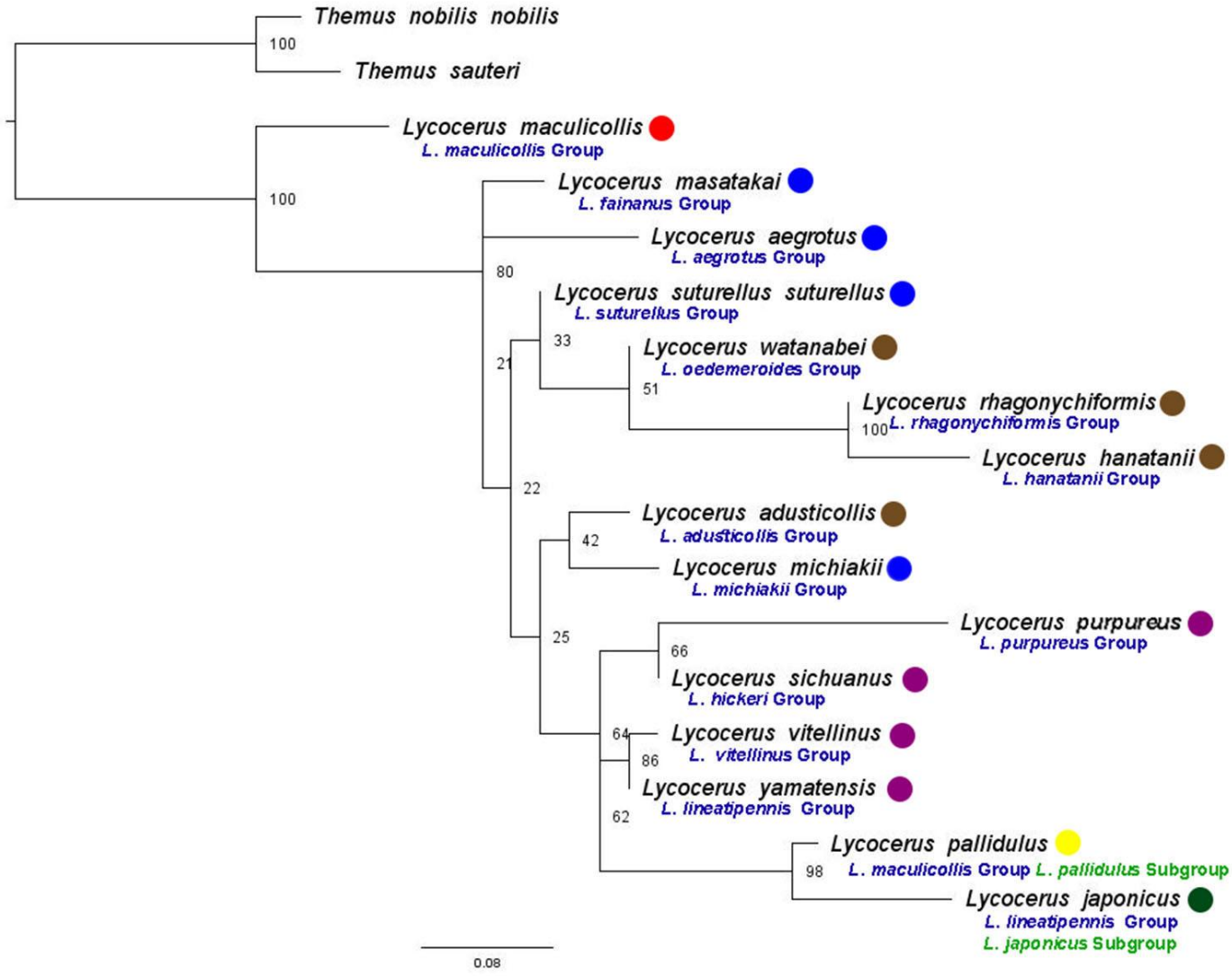

Figure 4. Maximum Likelihood phylogenetic tree of *Lycocerus* based on 46 morphological characters. Circles after species names indicate the genus/subgenus based on Wittmer's classification, showing the non-monophyly: red circle: *Lycocerus*; blue circles: *Athemus* (*Athemus*); brown circles: *Athemus* (*Athemellus*); purple circles: *Athemus* (*Andrathemus*); yellow circles: *Athemus* (*lsathemus*); dark green circles: *Athemus* (*Mikadocantharis*).

The type species of *Lycocerus* and *Athemus* can be easily distinguished from each other by characteristics of the antennae, vertex of the head, pronotum, male genitalia and the eighth abdominal sternite of females (Kasantsev, 1999), and it is thus seemingly reasonable to separate them into different genera. However, Okushima (2005) noted that these plausible diagnostic characteristics fail to apply for all *Lycocerus* and *Athemus* species and argued that a broadly defined genus, inclusive of these characteristics should be proposed, and thus two genera were synonymized. In the present phylogenies, despite the clear separation between *Lycocerus* and *Athemus* by several characters, the extremely low BS support values in MP and PP in BI, and weakly supported BS in ML still suggest that it is premature to separate the two genera without providing another objective evidence for this nomenclatural act.

Athemus Lewis, the junior synonym of *Lycocerus*, was one of the largest genera of Asian cantharids. It was divided into several subgenera (i.e. *Athemus*, *Andrathemus* Wittmer, *Athemellus* Wittmer, *lsathemus* Wittmer and *Mikadocantharis* Wittmer & Magis) based ondifferences only in the shape of the claws. With the consideration of all external characteristics and genitalic structures, Okushima (2005) indicated that the division based on the morphology of claws was artificial and should be synonymized. My analyses using morphological characters under various algorithms also reveal this unnatural subgeneric classification, with apparent non-monophyletic *Athemus*, *Andrathemus* and *Athemellus* (Figs 1–4), and thus support Okushima (2005)'s treatment.

Okushima & Hsiao (2017) upgraded *L. fainanus* Subgroup (*L. vitellinus* Group) to an independent species group based on its unique characteristics, namely large sized body, metallic elytra, and median lobe with a conspicuous process, which is supported by the present results as well. Additionally, these results indicate the distinct systematic position of the *L. pallidulus* Subgroup in the *L. maculicollis* Group and *L. japonicus* Subgroup in the *L. lineatipennis* Group, suggesting future investigation on the systematics

of other *Lycocerus* subgroups is required. The study herein provides a new insight into the phylogenetic relationship of a highly speciose genus of Asian Cantharidae.

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異菊虎屬系統分類學初探（鞘翅目：菊虎科）

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摘要: 異菊虎屬 (*Lycocerus* Gorham, 1889) 是多樣性極高的亞洲產菊虎類群。Okushima (2005) 將本屬劃分成數個種群並基於形態解剖比較推測異菊虎屬內的親緣關係，此後又有數位學者提出數個異菊虎種群。在本研究中，我們基於形態數據，透過系統發育分析重新探討異菊虎的屬內關係，並將取樣範圍延伸到目前已知主要的菊虎支系。分析結果與 Okushima (2005) 提出推測的樹型僅部分一致但支持其提出的異麗菊虎 (*Athemus* Lewis, 1895)、細身異麗菊虎 (*Athemellus* Wittmer, 1972)、米卡菊虎 (*Mikadocantharis* Wittmer & Magis, 1978)、安卓麗菊虎 (*Andrathemus* Wittmer, 1978) 和伊斯麗菊虎 (*lsathemus* Wittmer, 1995) 為異菊虎的同物異名處理。

關鍵詞: 菊虎、菊虎亞科、系統學、形態系統發育學、亞洲

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臺灣錐頭螽利用人為砍伐之殘餘竹筒作為冬季棲所之觀察記述（直翅目：螽斯科）

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摘要: 臺灣錐頭螽 (*Pyrgocorypha formosana* Matsumura & Shiraki, 1908) 於冬季夜間成對棲息於苗栗縣西湖鄉一處人為砍伐後殘餘竹筒之觀察紀錄，並藉此觀察討論臺灣錐頭螽具有守衛配偶行為的可能性。

關鍵詞: 螽斯科、錐頭螽屬、冬季棲所、竹筒、守衛配偶

錐頭螽屬 (*Pyrgocorypha*) 的分類混亂且多依據於形態，Liu et al. (2012) 認為 *Pyrgocorypha formosana* 應為平刺錐頭螽 (*Pyrgocorypha planispina* (De Haan, 1842)) 之同物異名，並記述平刺錐頭螽分布於臺灣，然而該研究未引述採自臺灣的標本，Sri-in & Yang (2019) 仍視 *P. formosana* 為有效名，在直翅類學會網站 (Orthoptera Species File, 2020) 及物種名錄 (Catalogue of Life, 2020) 亦登錄為有效學名。本研究並未牽涉分類處理，故仍將臺灣產的錐頭螽視為 *P. formosana*。作者於 2020 年 12 月 17 日晚間 19:17 於苗栗縣西湖鄉進行生態調查，當日天氣晴朗，氣溫為 19.4℃，於綠竹 (*Bambusa oldhamii* Munro, 1868) 竹筒內發現臺灣錐頭螽，記錄周圍環境及生物棲息情形，照片均以 iPhone SE2 之照相功能拍攝，隨後採集引證標本，存放於作者收藏 (PWC: P.-W. Chen's private collection, Taipei, Taiwan)。

觀察環境為一鄰近竹闊混合林之竹叢，周圍有草生地及乾涸埤塘鑲嵌 (圖一 A)。有多個竹莖於大約胸高處有機械性砍伐切口，殘餘部分自竹節以上枯死，長約 25 公分 (圖一 B)。自砍伐切口觀察，發現臺灣錐頭螽 1 雌 1 雄成蟲停棲於竹筒靠近底部之內壁，兩隻臺灣錐頭螽雖不相接觸但彼此距離近，頭部均朝向砍伐切口，觸角向後貼齊身體。該竹筒內尚有黑竹緣椿象 (*Notobitus meleagris* (Fabricius, 1787)) 及疣尾蝎虎 (*Hemidactylus frenatus* Schlegel, 1836) 各 1 隻 (圖一 C)。於觀察地點其他人為砍伐竹筒發現 4 隻群聚的黑竹緣椿象 (圖二 A) 及竹筒底部的昆蟲卵 (圖二 B) 、中國樹蟾 (*Hyla chinensis* Guenther, 1858) (圖二 C) 、疣尾蝎虎 (圖二 D) 等動物利用。

螽斯科的成員在不活動時偏好利用植物作為休息處 (Gwynne, 2001)，例如草叢、葉鞘縫隙、樹洞、樹皮下等，然而臺灣產的螽斯種類鮮少有與其相關植物的紀錄，藏匿棲所的紀錄更是缺乏。Sri-in & Yang (2015) 記述臺灣錐頭螽的棲地為果園、次生林、開闊林地的灌叢；葉宗哲先生曾於 2015 年 6 月於 Facebook 社團「直翅目生態貼圖發問區」發表臺灣錐頭螽於竹子的葉鞘產卵照片 (葉，私人通訊)，顯示本種至少於繁殖期間與竹子植株相關。錐頭螽所屬的草螽亞科 (Conocephalinae) 凹額草螽族 (Copiphorini) 有數個種類已確認會以成蟲階段過冬 (Kim & Kim, 2002)，而竹筒可能正好提供較溫和的微氣候條件，或提供庇護以躲避捕食者。在觀察地點許多竹筒均有動物棲息甚至繁殖 (圖二)，包括本觀察中錐頭螽棲息的竹筒也有其他動物共棲 (圖一 C、D)，顯示竹筒可能為當地動物重要而稀缺的藏匿處，而人為的局部砍伐在此案例中無意間提供了動物度冬棲所。本次觀察的錐頭螽為雌雄一對共棲於同一竹筒內，許多昆蟲包含直翅目在內均有觀察過守衛配偶 (mate-guarding) 之行為 (Alcock, 1994)，Ü nal & Beccaloni (2017) 報導了馬達加斯加數種草螽亞科的螽斯成對棲息於掩蔽處的現象，並提出可能是首次於螽斯科觀察到的守衛配偶行為，與本次於錐頭螽觀察的情形類似。然而葉 (2015) 的產卵觀察時為夏季，冬季可能非臺灣錐頭螽的繁殖季節，這可能顯示臺灣錐頭螽於非繁殖季節依然維持配偶關係，抑或此二個體並非配偶，僅是碰巧選擇了同一棲所，尚待未來針對其生活史的觀察方能釐清。

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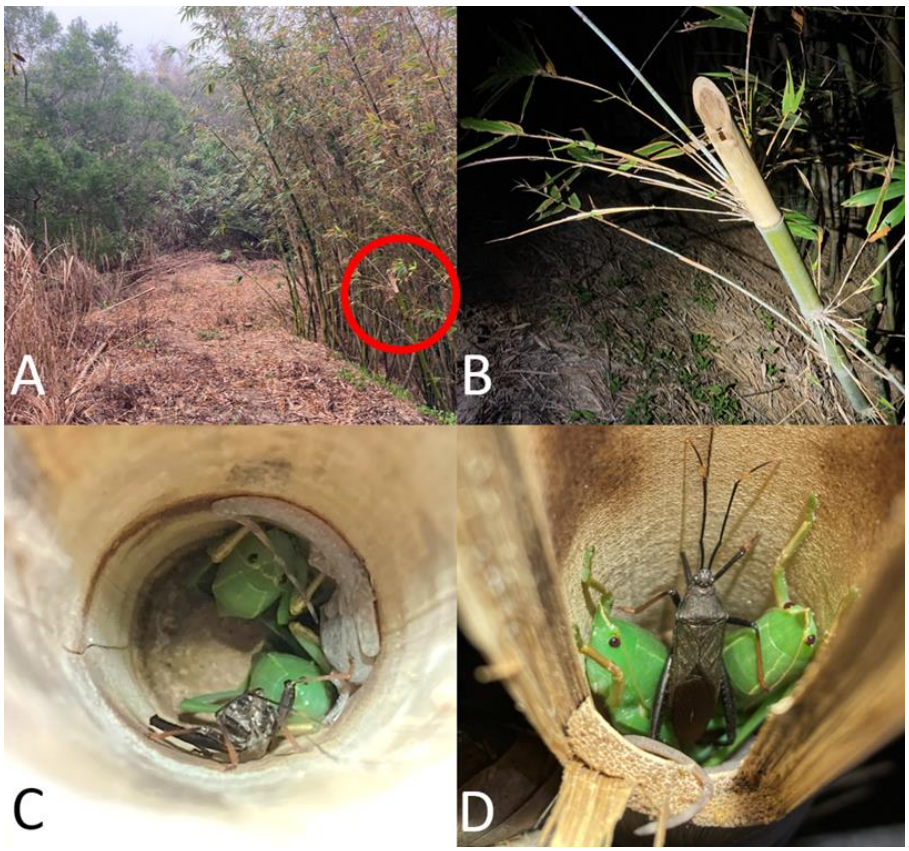
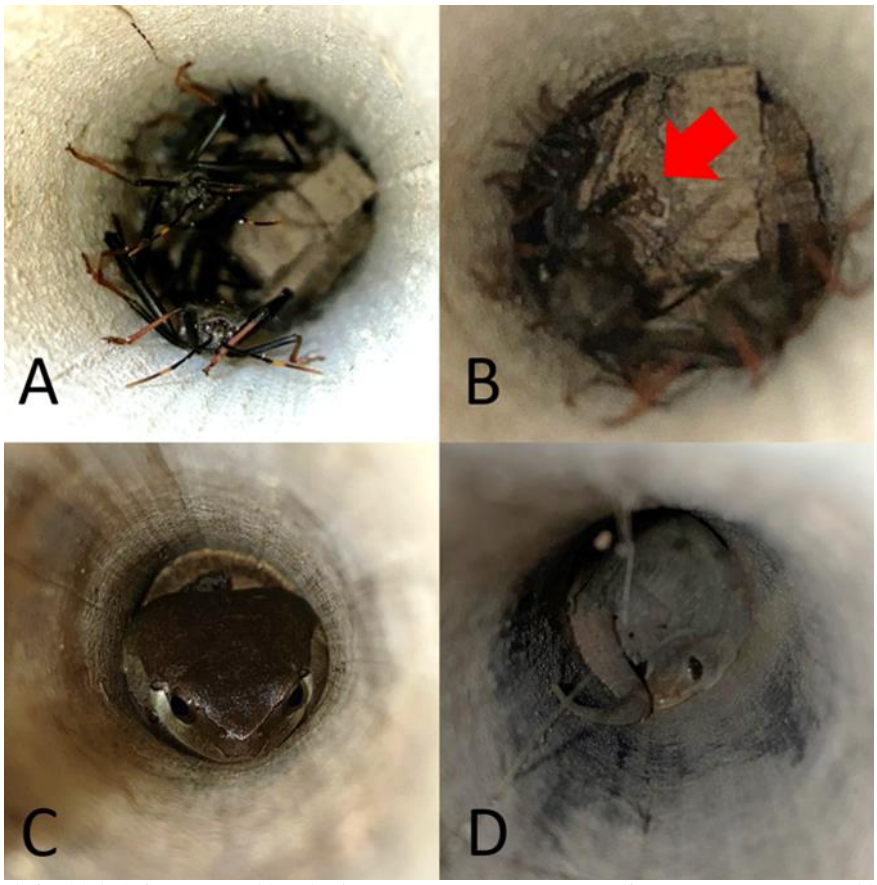


圖一、臺灣錐頭螽 (*Pyrgocorypha formosana*) 利用竹筒作為棲所：A. 觀察環境，紅色圓圈內為觀察竹筒位置；B. 頂端遭人為砍伐的殘餘竹筒；C. 從竹筒切口觀察，可見臺灣錐頭螽、黑竹緣椿象、疣尾蝎虎；D. 作者將部份竹筒拆除以便觀察。



圖二、其他利用竹筒作為棲所的動物：A. 黑竹緣椿象 (*Notobitus meleagris*) 群聚；B. 同 A，顯示竹筒底部的昆蟲卵 (紅色箭頭所指)；C. 中國樹蟾 (*Hyla chinensis*)；D. 疣尾蝎虎 (*Hemidactylus frenatus*)。

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Notes on *Pyrgocorypha formosana* (Orthoptera: Tettigoniidae) Hiding in an Artificially Cut Bamboo Stump as a Harbourage in Winter

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Abstract. An observational record of a pair of *Pyrgocorypha formosana* Matsumura & Shiraki, 1908 found hiding inside an artificially cut bamboo stump as refuge on a winter night in Xihu Township, Miaoli County, Taiwan is provided. The discussion of potential mate-guarding behaviour in this species is also provided.

Key words: Tettigoniidae, *Pyrgocorypha*, winter refuge, bamboo stump, mate-guarding

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